

**IN THE CLAIMS:**

Please amend claims 1-3, 5-6, 8 and 12 as follows:

1. (Currently Amended) A method for displaying a dendrogram comprising the steps of:  
    clustering a plurality of biopolymers with a first clustering method which is  
    based on a set of gene expression data obtained by experiments ~~under different~~  
    ~~conditions~~ on the plurality of biopolymers, and displaying clustering results thereof in  
    a form of a dendrogram in a display window;  
    selecting a subtree in the dendrogram in the display window;  
    displaying the selected subtree in a separate display window;  
    grouping biopolymers in the selected subtree in the separate display window  
    into at least one function group sharing a common one of functional characteristics  
    including enzymatic, metabolic, transporting, and cell cycle functions; and  
    displaying said function group of biopolymers in the separate display window.
2. (Currently Amended) A method for displaying a dendrogram according to claim 1,  
    further comprising the steps of:  
    designating a ~~different~~ second clustering method, which is different from the  
    first clustering method, for further clustering the biopolymers in the selected subtree  
    in the separate display window ~~said grouping step.~~
3. (Currently Amended) A method for displaying a dendrogram comprising the steps of:  
    clustering a plurality of biopolymers based on a set of gene expression data  
    obtained by experiments ~~under different conditions~~ on the plurality of biopolymers,  
    and displaying clustering results thereof in a form of a dendrogram in a display  
    window;  
    selecting a subtree in the dendrogram in the display window;  
    replacing the selected subtree with an icon in the dendrogram thereby  
    displaying the dendrogram with the icon rather than with the selected subtree  
    ~~simplifying a presentation in the display window;~~  
    grouping biopolymers in the simplified presentation in the display window  
    into at least one function group sharing a common one of functional characteristics

including enzymatic, metabolic, transporting, and cell cycle functions; and

displaying said function group of biopolymers in the simplified presentation in the display window.

4. (Previously Presented) A method for displaying a dendrogram according to claim 3, further comprising a step of restoring the selected subtree back from the replacing icon in the dendrogram in the display window.

5. (Currently Amended) A method for displaying a dendrogram comprising the steps of:  
clustering a plurality of biopolymers based on a set of gene expression data obtained by experiments ~~under different conditions~~ on the plurality of biopolymers, and displaying clustering results thereof in a form of a dendrogram in a display window;

selecting a subtree in the dendrogram in the display window;

~~selecting~~ searching in the selected subtree for keywords [[from]] available in a keyword dictionary file; and

counting biopolymers in the selected subtree whose biopolymer information contains at least one of the ~~selected~~ searched keywords available in the selected subtree and displaying each of the ~~selected~~ searched keywords available in the selected subtree with a corresponding count of the biopolymers whose biopolymer information contains at least one of the ~~selected~~ searched keywords available in the selected subtree;

grouping biopolymers in the selected subtree into at least one function group sharing a common one of functional characteristics including enzymatic, metabolic, transporting, and cell cycle functions;

displaying said function group of biopolymers in the display window; and

displaying the ~~selected~~ searched keywords available in the selected subtree and said count in a separated display window on top of the display window displaying said function group of biopolymers therein;

highlighting in the display window a location of each of the biopolymers in the selected subtree whose biopolymer information contains the searched keywords available in the selected subtree;

displaying the highlighted keywords together with said function group of

biopolymers thereby confirming ~~relative~~ biopolymers sharing the common one of said functional characteristics are ~~assembled~~ grouped in the selected subtree,

wherein said biopolymer information includes a unique nucleotide sequence identifier and a description of a corresponding nucleotide sequence, said description includes a source organism, a gene name/protein name, or a function.

6. (Currently Amended) A method for displaying a dendrogram comprising the steps of:

clustering a plurality of biopolymers based on a set of gene expression data obtained by experiments ~~under different conditions~~ on the plurality of biopolymers, and displaying clustering results thereof in a form of a dendrogram in a display window;

selecting a subtree in the dendrogram in the display window;

designating at least one keyword from a keyword dictionary file;

searching in the selected subtree for biopolymers whose biopolymer information contains the designated keyword; and

highlighting in the display window a location of each of the biopolymers in the selected subtree whose biopolymer information contains the designated keyword;

grouping biopolymers in the selected subtree into at least one function group sharing a common one of functional characteristics including enzymatic, metabolic, transporting, and cell cycle functions;

displaying the highlighted keywords together with said function group of biopolymers in the display window thereby confirming ~~relative~~ biopolymers sharing the common one of said functional characteristics are ~~assembled~~ grouped in the selected subtree,

wherein said biopolymer information includes a unique nucleotide sequence identifier and a description of a corresponding nucleotide sequence, said description includes a source organism, a gene name/protein name, or a function.

7. (Original) A method for displaying a dendrogram according to any one of claims 1 to 6, wherein the biopolymers are cDNAs, RNAs, DNA fragments or genes.

8. (Currently Amended) A system for displaying a dendrogram comprising:
  - a clustering processor for clustering a plurality of biopolymers based on a set of gene expression data obtained by experiments ~~under different conditions~~ on the plurality of biopolymers, and analyzing and displaying clustering results thereof in a form of a dendrogram in a display window;
  - a display system for displaying the dendrogram, for displaying on a separate window a subtree selected by a user in the display window thereby grouping biopolymers in the selected subtree in the separate display window into at least one function group sharing a common one of functional characteristics including enzymatic, metabolic, transporting, and cell cycle functions, and for displaying said function group of biopolymers in the separate display window; and
  - a keyword dictionary file for storing keywords of biopolymer information associated with each of the plurality of biopolymers, said biopolymer information including a unique nucleotide sequence identifier and a description of a corresponding nucleotide sequence, said description includes a source organism, a gene name/protein name, or a function.
9. (Previously Presented) A system for displaying a dendrogram according to claim 8, further comprising input means for selecting the subtree by the user.
10. (Previously Presented) A system for displaying a dendrogram according to claim 8, further comprising means for designating a different clustering method for said grouping biopolymers in the selected subtree displayed on the separate window to secondarily cluster biopolymers included in the subtree, wherein the display system displays secondarily clustered biopolymers in the selected subtree in a form of a dendrogram.
11. (Previously Presented) A system for displaying a dendrogram according to any one of claims 8 to 10, further comprising means for replacing the selected subtree with an icon, and means for restoring the selected subtree back from the replacing icon in the dendrogram in the display window.

12. (Currently Amended) A system for displaying a dendrogram according to any one of claims 8 to 10, further comprising means for ~~retrieving~~ designating keywords from the keyword dictionary file, means for counting biopolymers in the subtree whose biopolymer information contains at least one of the retrieved keywords, wherein the display system displays each of the ~~retrieved~~ designated keywords with a corresponding count of the biopolymers whose biopolymer information contains at least one of the ~~retrieved~~ designated keywords, and highlights a location of each of the biopolymers in the selected subtree whose biopolymer information contains at least one of the ~~retrieved~~ designated.
13. (Previously Presented) A system for displaying a dendrogram according to any one of claims 8 to 10, wherein the biopolymers are cDNAs, RNAs, DNA fragments or genes.
14. (Previously Presented) A method for displaying a dendrogram according to claim 5, wherein the counting step involves counting biopolymers in the selected subtree whose biopolymer information contains synonyms of said one of the selected keywords.
15. (Previously Presented) A system for displaying a dendrogram according to claim 12, wherein the means for counting counts biopolymers in the selected subtree whose biopolymer information contains synonyms of each of the retrieved keywords.